Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

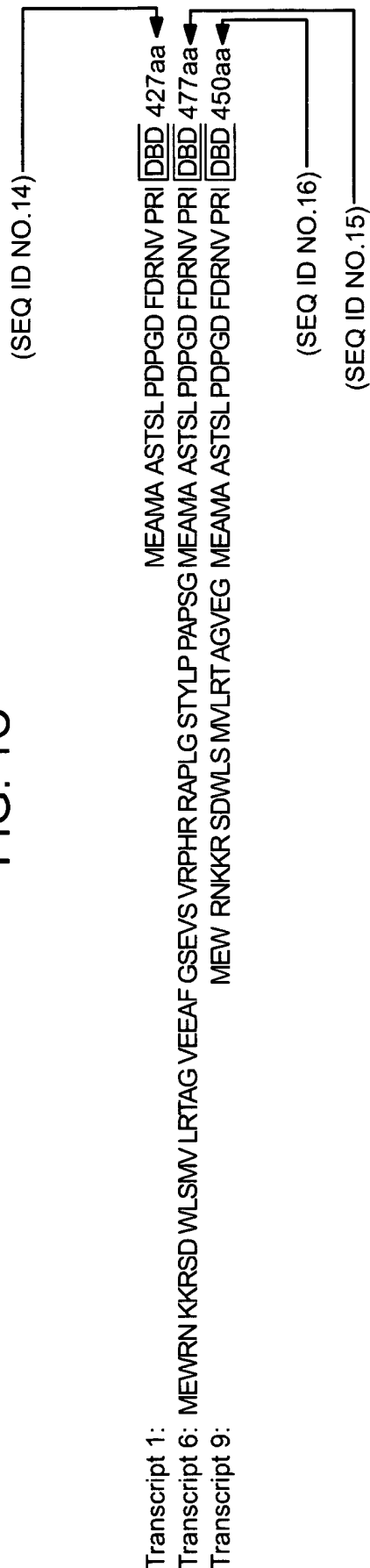**FIG.1A**

Exons: 1f   1e 1a 1d 1b   1c 2   3   45678 9
Cosmids: J5 ———————— AE ———————— D2 —— WE

FIG.1B

Title: "ISOFORMS OF THE HUMAN VITAMIN D RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

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FIG. 1C

Transcript 1:

Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI DBD 427aa

Transcript 9: MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNV PRI DBD 450aa

MEAMA ASTSL PDPGD FDRNV PRI DBD 477aa

(SEQ ID NO.14)

(SEQ ID NO.16)

(SEQ ID NO.15)

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FIG. 2

Title: "ISOFORMS OF THE HUMAN VITAMIN D
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FIG. 3

A.

1kb

1a   1d

Mean Luciferase Activity (% of 1a(-488,+75)±SEM)

0   20   40   60   80   100

1a(-898,+75)

1a(-488,+75)

1a(-317,+75)

1a(-94,+75)

1a(-29,+75)

1d(+87,+424)

1d(+244,+424)

1a-1d(-846,+470)

1a-1d(-846,+243)

1a-1d(-94,+470)

1a-1d(-94,+243)

B.

1f

Mean Luciferase Activity (% of 1a(-488,+75)±SEM)

0   10   20   30

1f(-1168,+58)

1f(-606,+58)

1f(-278,+58)

1f(-172,+58)

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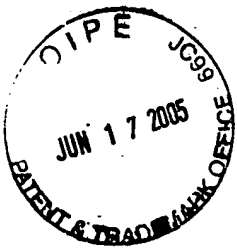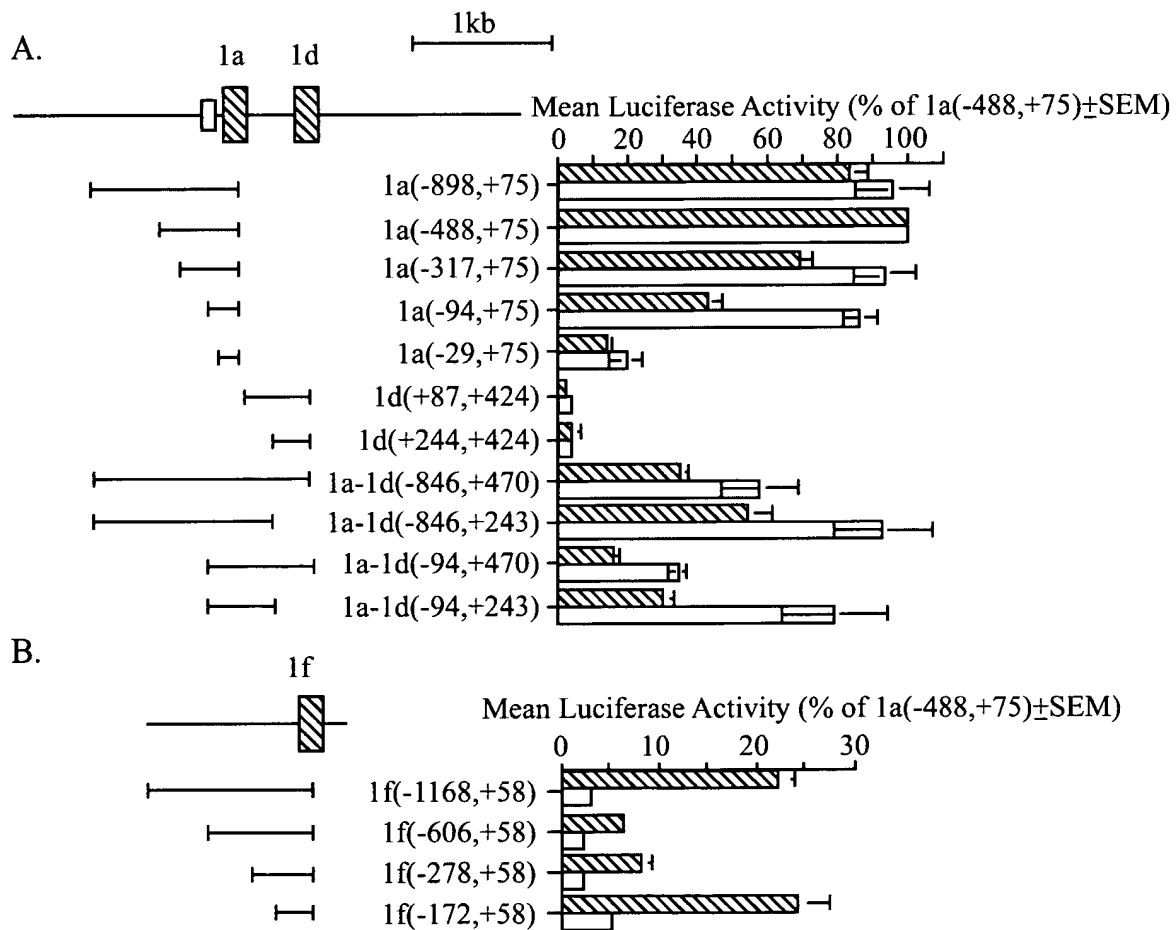Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 4

A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

C. 5'...tgtttttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGC ATG GAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCG ATG GTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 22)

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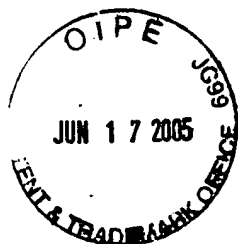# FIG. 5A

Transcript 6
(Sequence Range: 1 to 1463)

```
             10         20         30         40         50
          *    *     *    *     *    *     *    *     *    *
        GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
        CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                          MetGluTrpArg AsnLysLys>


             60         70         80         90        100
          *    *     *    *     *    *     *    *     *    *
        AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
        TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
        ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>


            110        120        130        140        150
          *    *     *    *     *    *     *    *     *    *
        CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
        GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
         PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>


            160        170        180        190        200
          *    *     *    *     *    *     *    *     *    *
        CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
        GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
        SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>


            210        220        230        240        250
          *    *     *    *     *    *     *    *     *    *
        ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
        TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
        ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>


            260        270        280        290        300
          *    *     *    *     *    *     *    *     *    *
        TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
        ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
        GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>


            310        320        330        340        350
          *    *     *    *     *    *     *    *     *    *
        GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
        CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
        CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>


            360        370        380        390        400
          *    *     *    *     *    *     *    *     *    *
        TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
        AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
        PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

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REPLACEMENT SHEET

FIG. 5B

```
            410        420        430        440        450
       *     *    *     *    *     *    *     *    *     *
     CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
     GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
      HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>


            460        470        480        490        500
       *     *    *     *    *     *    *     *    *     *
     AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
     TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
     LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>


            510        520        530        540        550
       *     *    *     *    *     *    *     *    *     *
     CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
     GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
     LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>


            560        570        580        590        600
       *     *    f     *    *     *    *     *    *     *
     GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
     CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
      SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>


            610        620        630        640        650
       *     *    *     *    *     *    *     *    *     *
     AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
     TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
     LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>


            660        670        680        690        700
       *     *    *     *    *     *    *     *    *     *
     CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
     GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
     ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>


            710        720        730        740        750
       *     *    *     *    *     *    *     *    *     *
     CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
     GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
      ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>


            760        770        780        790        800
       *     *    *     *    *     *    *     *    *     *
     TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
     AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
     IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>


            810        820        830        840        850
       *     *    *     *    *     *    *     *    *     *
     AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
     TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
     SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```
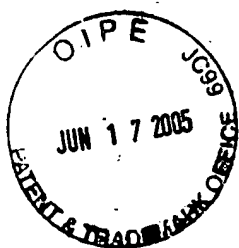
Title: "ISOFORMS OF THE HUMAN VITAMIN D
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Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 5C

```
       860        870        880        890        900
    *     *    *     *    *     *    *     *    *     *
uCTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
 GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu  ProHisLeu  AlaAspLeuVal SerTyrSer  IleGlnLys>


       910        920        930        940        950
    *     *    *     *    *     *    *     *    *     *
 TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
 AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
 ValIleGlyPhe AlaLysMet  IleProGly  PheArgAspLeu ThrSerGlu>


       960        970        980        990        1000
    *     *    *     *    *     *    *     *    *     *
 GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
 CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
 AspGlnIle  ValLeuLeuLys SerSerAla IleGluVal  IleMetLeuArg>


      1010       1020       1030       1040       1050
    *     *    *     *    *     *    *     *    *     *
 CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
 GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu  SerPheThr  MetAspAspMet SerTrpThr  CysGlyAsn>


      1060       1070       1080       1090       1100
    *     *    *     *    *     *    *     *    *     *
 AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
 TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
 GlnAspTyrLys TyrArgVal  SerAspVal  ThrLysAlaGly HisSerLeu>


      1110       1120       1130       1140       1150
    *     *    *     *    *     *    *     *    *     *
 GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
 CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
 GluLeuIle  GluProLeuIle LysPheGln  ValGlyLeu  LysLysLeuAsn>


      1160       1170       1180       1190       1200
    *     *    *     *    *     *    *     *    *     *
 CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
 GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
 LeuHisGlu  GluGluHis  ValLeuLeuMet AlaIleCys  IleValSer>


      1210       1220       1230       1240       1250
    *     *    *     *    *     *    *     *    *     *
 CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
 GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
 ProAspArgPro GlyValGln  AspAlaAla  LeuIleGluAla IleGlnAsp>


      1260       1270       1280       1290       1300
    *     *    *     *    *     *    *     *    *     *
 CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
 GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
 ArgLeuSer  AsnThrLeuGln ThrTyrIle  ArgCysArg  HisProProPro>
```

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Application No.: 09/509,482
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REPLACEMENT SHEET
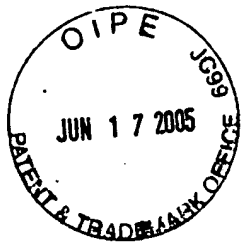
FIG. 5D

```
           1310         1320         1330         1340         1350
         *     *      *     *      *     *      *     *      *     *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
 GlySerHis  LeuLeuTyr  AlaLysMetIle GlnLysLeu  AlaAspLeu>


           1360         1370         1380         1390         1400
         *     *      *     *      *     *      *     *      *     *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis  SerLysGln  TyrArgCysLeu SerPheGln>


           1410         1420         1430         1440         1450
         *     *      *     *      *     *      *     *      *     *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
 ProGluCys  SerMetLysLeu ThrProLeu  ValLeuGlu  ValPheGlyAsn>


           1460
         *     *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
 GluIleSer  ***>(SEQ ID NO:9)
```

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REPLACEMENT SHEET

FIG. 6A

Transcript 9
(Sequence range: 1 to 1382)

```
           10        20        30        40        50
      *    *    *    *    *    *    *    *    *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                MetGluTrpArg AsnLysLys>


           60        70        80        90        100
      *    *    *    *    *    *    *    *    *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>


           110       120       130       140       150
      *    *    *    *    *    *    *    *    *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>


           160       170       180       190       200
      *    *    *    *    *    *    *    *    *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>


           210       220       230       240       250
      *    *    *    *    *    *    *    *    *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>


           260       270       280       290       300
      *    *    *    *    *    *    *    *    *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
 MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>


           310       320       330       340       350
      *    *    *    *    *    *    *    *    *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>


           360       370       380       390       400
      *    *    *    *    *    *    *    *    *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

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REPLACEMENT SHEET

FIG. 6B

```
           410        420        430        440        450
        *     *     *     *     *     *     *     *     *     *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
ArgLysArg  GluMetIle  LeuLysArgLys GluGluGlu AlaLeuLys>


           460        470        480        490        500
        *     *     *     *     *     *     *     *     *     *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>


           510        520        530        540        550
        *     *     *     *     *     *     *     *     *     *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>


           560        570        580        590        600
        *     *     *     *     *     *     *     *     *     *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
 GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>


           610        620        630        640        650
        *     *     *     *     *     *     *     *     *     *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>


           660        670        680        690        700
        *     *     *     *     *     *     *     *     *     *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>


           710        720        730        740        750
        *     *     *     *     *     *     *     *     *     *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
 PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>


           760        770        780        790        800
        *     *     *     *     *     *     *     *     *     *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>


           810        820        830        840        850
        *     *     *     *     *     *     *     *     *     *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
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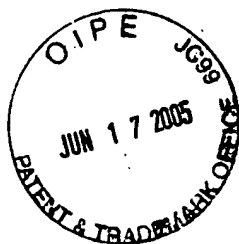
Title: "ISOFORMS OF THE HUMAN VITAMIN D RECEPTOR"
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Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 6C

```
          860         870         880         890         900
      *      *     *      *     *      *     *      *     *      *
   CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
   GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
   ArgAspLeu  ThrSerGlu  AspGlnIleVal LeuLeuLys  SerSerAla>


          910         920         930         940         950
      *      *     *      *     *      *     *      *     *      *
   TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
   AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
   IleGluValIle MetLeuArg  SerAsnGlu  SerPheThrMet AspAspMet>


          960         970         980         990         1000
      *      *     *      *     *      *     *      *     *      *
   TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
   AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
   SerTrpThr  CysGlyAsnGln AspTyrLys  TyrArgVal  SerAspValThr>


          1010        1020        1030        1040        1050
      *      *     *      *     *      *     *      *     *      *
   CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
   GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
   LysAlaGly  HisSerLeu  GluLeuIleGlu ProLeuIle  LysPheGln>


          1060        1070        1080        1090        1100
      *      *     *      *     *      *     *      *     *      *
   TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
   ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
   ValGlyLeuLys LysLeuAsn  LeuHisGlu  GluGluHisVal LeuLeuMet>


          1110        1120        1130        1140        1150
      *      *     *      *     *      *     *      *     *      *
   GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
   CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
   AlaIleCys  IleValSerPro AspArgPro  GlyValGln  AspAlaAlaLeu>


          1160        1170        1180        1190        1200
      *      *     *      *     *      *     *      *     *      *
   GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
   CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
   IleGluAla  IleGlnAsp  ArgLeuSerAsn ThrLeuGln  ThrTyrIle>


          1210        1220        1230        1240        1250
      *      *     *      *     *      *     *      *     *      *
   GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
   CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
   ArgCysArgHis ProProPro  GlySerHis  LeuLeuTyrAla LysMetIle>


          1260        1270        1280        1290        1300
      *      *     *      *     *      *     *      *     *      *
   CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
   GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
   GlnLysLeu  AlaAspLeuArg SerLeuAsn  GluGluHis  SerLysGlnTyr>
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 6D

```
          1310       1320       1330       1340       1350
       *      *      *      *      *      *      *      *      *      *
     CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
     GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
     ArgCysLeu  SerPheGln  ProGluCysSer MetLysLeu  ThrProLeu>


          1360       1370       1380
       *      *      *      *      *      *
     TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA  (SEQ ID NO:3)
     ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT  (SEQ ID NO:18)
     ValLeuGluVal PheGlyAsn GluIleSer ***>  (SEQ ID NO:10)
```

REPLACEMENT SHEET

FIG. 7A

Transcript 10
(Sequence Range: 1 to 1534)

```
            10        20        30        40        50
        *    *    *    *    *    *    *    *    *    *
    GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
    CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                     MetGluTrpArg AsnLysLys>


            60        70        80        90        100
        *    *    *    *    *    *    *    *    *    *
    AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
    TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
    ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>


            110       120       130       140       150
        *    *    *    *    *    *    *    *    *    *
    GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
    CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
     GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>


            160       170       180       190       200
        *    *    *    *    *    *    *    *    *    *
    GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
    CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
    ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>


            210       220       230       240       250
        *    *    *    *    *    *    *    *    *    *
    CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
    GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
    HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***(SEQ ID NO:11)


            260       270       280       290       300
        *    *    *    *    *    *    *    *    *    *
    CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
    GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC


            310       320       330       340       350
        *    *    *    *    *    *    *    *    *    *
    TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
    AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA


            360       370       380       390       400
        *    *    *    *    *    *    *    *    *    *
    CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
    GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 7B

```
          410        420        430        440        450
       *     *    *     *    *     *    *     *    *     *
    AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
    TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC


          460        470        480        490        500
       *     *    *     *    *     *    *     *    *     *
    CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
    GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA


          510        520        530        540        550
       *     *    *     *    *     *    *     *    *     *
    GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
    CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC


          560        570        580        590        600
       *     *    *     *    *     *    *     *    *     *
    CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
    GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT


          610        620        630        640        650
       *     *    *     *    *     *    *     *    *     *
    GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
    CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT


          660        670        680        690        700
       *     *    *     *    *     *    *     *    *     *
    TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
    ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG


          710        720        730        740        750
       *     *    *     *    *     *    *     *    *     *
    TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
    ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG


          760        770        780        790        800
       *     *    *     *    *     *    *     *    *     *
    TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
    AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA


          810        820        830        840        850
       *     *    *     *    *     *    *     *    *     *
    CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
    GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG


          860        870        880        890        900
       *     *    *     *    *     *    *     *    *     *
    AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
    TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA


          910        920        930        940        950
       *     *    *     *    *     *    *     *    *     *
    GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
    CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 7C

```
          960         970         980         990        1000
       *     *     *     *     *     *     *     *     *     *
     TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
     AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT


         1010        1020        1030        1040        1050
       *     *     *     *     *     *     *     *     *     *
     TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
     AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG


         1060        1070        1080        1090        1100
       *     *     *     *     *     *     *     *     *     *
     CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
     GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT


         1110        1120        1130        1140        1150
       *     *     *     *     *     *     *     *     *     *
     TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
     ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC


         1160        1170        1180        1190        1200
       *     *     *     *     *     *     *     *     *     *
     ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
     TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT


         1210        1220        1230        1240        1250
       *     *     *     *     *     *     *     *     *     *
     GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
     CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT


         1260        1270        1280        1290        1300
       *     *     *     *     *     *     *     *     *     *
     TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
     ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC


         1310        1320        1330        1340        1350
       *     *     *     *     *     *     *     *     *     *
     CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
     GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA


         1360        1370        1380        1390        1400
       *     *     *     *     *     *     *     *     *     *
     CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
     GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT


         1410        1420        1430        1440        1450
       *     *     *     *     *     *     *     *     *     *
     TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
     AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC


         1460        1470        1480        1490        1500
       *     *     *     *     *     *     *     *     *     *
     TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
     ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

REPLACEMENT SHEET

FIG. 7D

```
        1510        1520        1530
     *      *      *      *      *      *
  TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
  ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
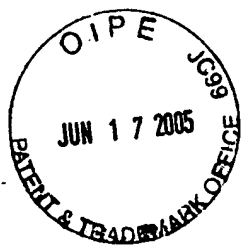Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 8A

```
           10          20          30          40          50
            *           *           *           *           *
      TGCGACCTTG  GCGGTGAGCC  TGGGGACAGG  GGTGAGGCCA  GAGACGGACG
      ACGCTGGAAC  CGCCACTCGG  ACCCCTGTCC  CCACTCCGGT  CTCTGCCTGC


           60          70          80          90         100
            *           *           *           *           *
      GACGCAGGGG  CCCGGCCCAA  GGCGAGGGAG  AACAGCGGCA  CTAAGGCAGA
      CTGCGTCCCC  GGGCCGGGTT  CCGCTCCCTC  TTGTCGCCGT  GATTCCGTCT


          110         120         130         140         150
            *           *           *           *           *
      AAGGAAGAGG  GCGGTGTGTT  CACCCGCAGC  CCAATCCATC  ACTCAGCAAC
      TTCCTTCTCC  CGCCACACAA  GTGGGCGTCG  GGTTAGGTAG  TGAGTCGTTG


          160         170         180         190         200
            *           *           *           *           *
      TCCTAGACGC  TGGTAGAAAG  TTCCTCCGAG  GAGCCTGCCA  TCCAGTCGTG
      AGGATCTGCG  ACCATCTTTC  AAGGAGGCTC  CTCGGACGGT  AGGTCAGCAC


          210         220         230         240         250
            *           *           *           *           *
      CGTGCAGAAG  CCTTTGGGTC  TGAAGTGTCT  GTGAGACCTC  ACAGAAGAGC
      GCACGTCTTC  GGAAACCCAG  ACTTCACAGA  CACTCTGGAG  TGTCTTCTCG


          260         270         280         290         300
            *           *           *           *           *
      ACCCCTGGGC  TCCACTTACC  TGCCCCCTGC  TCCTTCAGGG  ATGGAGGCAA
      TGGGGACCCG  AGGTGAATGG  ACGGGGGACG  AGGAAGTCCC  TACCTCCGTT
                                                      MetGluAla>


          310         320         330         340         350
            *           *           *           *           *
      TGGCGGCCAG  CACTTCCCTG  CCTGACCCTG  GAGACTTTGA  CCGGAACGTG
      ACCGCCGGTC  GTGAAGGGAC  GGACTGGGAC  CTCTGAAACT  GGCCTTGCAC
      MetAlaAlaSer ThrSerLeu  ProAspPro  GlyAspPheAsp ArgAsnVal>


          360         370         380         390         400
            *           *           *           *           *
      CCCCGGATCT  GTGGGGTGTG  TGGAGACCGA  GCCACTGGCT  TTCACTTCAA
      GGGGCCTAGA  CACCCCACAC  ACCTCTGGCT  CGGTGACCGA  AAGTGAAGTT
      ProArgIle  CysGlyValCys GlyAspArg  AlaThrGly  PheHisPheAsn>


          410         420         430         440         450
            *           *           *           *           *
      TGCTATGACC  TGTGAAGGCT  GCAAAGGCTT  CTTCAGGCGA  AGCATGAAGC
      ACGATACTGG  ACACTTCCGA  CGTTTCCGAA  GAAGTCCGCT  TCGTACTTCG
      AlaMetThr  CysGluGly  CysLysGlyPhe PheArgArg  SerMetLys>


          460         470         480         490         500
            *           *           *           *           *
      GGAAGGCACT  ATTCACCTGC  CCCTTCAACG  GGGACTGCCG  CATCACCAAG
      CCTTCCGTGA  TAAGTGGACG  GGGAAGTTGC  CCCTGACGGC  GTAGTGGTTC
      ArgLysAlaLeu PheThrCys  ProPheAsn  GlyAspCysArg IleThrLys>
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 8B

```
          510        520        530        540        550
           *          *          *          *          *
    GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
    CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
    AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

          560        570        580        590        600
           *          *          *          *          *
    CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
    GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
     GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

          610        620        630        640        650
           *          *          *          *          *
    GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
    CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
    ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

          660        670        680        690        700
           *          *          *          *          *
    CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
    GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
    ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

          710        720        730        740        750
           *          *          *          *          *
    CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
    GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
     AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

          760        770        780        790        800
           *          *          *          *          *
    GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
    CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
    ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

          810        820        830        840        850
           *          *          *          *          *
    AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
    TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
    AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

          860        870        880        890        900
           *          *          *          *          *
    AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
    TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
     AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

          910        920        930        940        950
           *          *          *          *          *
    ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
    TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
    AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

          960        970        980        990       1000
           *          *          *          *          *
    CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
    GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
    LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```
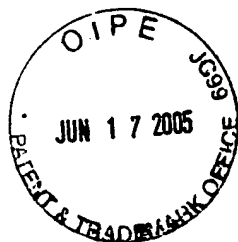
Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 8C

```
         1010       1020       1030       1040       1050
           *          *          *          *          *
     CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
     GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
      IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

         1060       1070       1080       1090       1100
           *          *          *          *          *
     TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
     AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
     LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

         1110       1120       1130       1140       1150
           *          *          *          *          *
     ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
     TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
     IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

         1160       1170       1180       1190       1200
           *          *          *          *          *
     CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
     GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
      CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

         1210       1220       1230       1240       1250
           *          *          *          *          *
     GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
     CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
     GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

         1260       1270       1280       1290       1300
           *          *          *          *          *
     AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
     TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
     LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

         1310       1320       1330       1340       1350
           *          *          *          *          *
     CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
     GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
      IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

         1360       1370       1380       1390       1400
           *          *          *          *          *
     CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
     GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
     AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

         1410       1420       1430       1440       1450
           *          *          *          *          *
     CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
     GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
     HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

         1460       1470       1480       1490       1500
           *          *          *          *          *
     AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
     TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
     AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"
Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

FIG. 8D
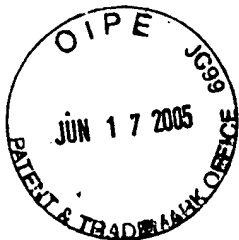
```
        1510         1520         1530         1540         1550
          *            *            *            *            *
    TCTCCTTCCA  GCCTGAGTGC  AGCATGAAGC  TAACGCCCCT  TGTGCTCGAA
    AGAGGAAGGT  CGGACTCACG  TCGTACTTCG  ATTGCGGGGA  ACACGAGCTT
    LeuSerPheGln ProGluCys  SerMetLys  LeuThrProLeu VALLeuGlu>
```

```
        1560         1570
          *            *
    GTGTTTGGCA  ATGAGATCTC  CTGA (SEQ ID NO:7)
    CACAAACCGT  TACTCTAGAG  GACT (SEQ ID NO:20)
    ValPheGly  AsnGluIleSer ***>(SEQ ID NO:12)
```